

GenCore Version 5.1.6  
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OM protein - protein search, using swi model

Run on: June 25, 2003, 14:38:41 ; Search time 25.6395 Seconds  
(without alignments)  
843.812 Million cell updates/sec

Title: US-09-622-613B-13

Perfect score: 582  
Sequence: 1 MSMLTFQKKHLNTRDVC.....TFCVTCENQAPVHFVGWGHG 105

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_proteob:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 573   | 98.5        | 127    | 13    | Q918V8      |
| 2          | 551   | 94.7        | 127    | 13    | Q8UYX5      |
| 3          | 399.5 | 68.6        | 129    | 13    | Q9DFY6      |
| 4          | 381   | 65.5        | 128    | 13    | Q9DFY8      |
| 5          | 306   | 53.6        | 128    | 13    | Q9DFY7      |
| 6          | 304   | 52.2        | 133    | 13    | Q9DFY5      |
| 7          | 293   | 50.3        | 133    | 13    | Q9DSM0      |
| 8          | 287   | 49.3        | 133    | 13    | Q9PMR7      |
| 9          | 281   | 48.3        | 132    | 13    | Q98SM2      |
| 10         | 281   | 48.3        | 133    | 13    | Q98SL9      |
| 11         | 277   | 47.6        | 133    | 13    | Q98SL8      |
| 12         | 275   | 47.3        | 132    | 13    | Q98SM1      |
| 13         | 270.5 | 46.5        | 132    | 13    | Q9DE78      |
| 14         | 157.5 | 27.1        | 169    | 13    | Q9W378      |
| 15         | 133   | 22.9        | 152    | 11    | Q9JKT5      |
| 16         | 131   | 22.5        | 157    | 11    | Q9JKT9      |

|    |       |      |     |    |        |             |
|----|-------|------|-----|----|--------|-------------|
| 17 | 130.5 | 22.4 | 153 | 11 | Q9JKT7 | mus saxicol |
| 18 | 130   | 22.3 | 157 | 11 | Q9JKT3 | meriones un |
| 19 | 127   | 21.8 | 154 | 11 | Q9JKT8 | mus saxicol |
| 20 | 127   | 21.8 | 157 | 11 | Q9JKT4 | meriones un |
| 21 | 126   | 21.6 | 157 | 11 | Q9JKT0 | meriones un |
| 22 | 125   | 21.5 | 157 | 11 | Q9JKT2 | meriones un |
| 23 | 124.5 | 21.4 | 155 | 11 | Q9JKT9 | mus pahari  |
| 24 | 123.5 | 21.2 | 155 | 11 | Q9JKT3 | mus saxicol |
| 25 | 120.5 | 20.7 | 155 | 11 | Q9JKT6 | mus saxicol |
| 26 | 119.5 | 20.5 | 155 | 11 | Q9JKT4 | mus saxicol |
| 27 | 119.5 | 20.5 | 155 | 11 | Q9JKT2 | mus saxicol |
| 28 | 117.5 | 20.2 | 155 | 11 | Q9JKT3 | rattus norv |
| 29 | 117   | 20.1 | 156 | 11 | Q9JKT7 | mus caroli  |
| 30 | 117   | 20.1 | 156 | 11 | Q9JKT6 | mus caroli  |
| 31 | 116.5 | 20.0 | 132 | 6  | Q9TV25 | eulemur ful |
| 32 | 116.5 | 20.0 | 132 | 6  | Q9TV24 | galago mo   |
| 33 | 116.5 | 20.0 | 155 | 11 | Q9JKT5 | mus musculu |
| 34 | 116.5 | 20.0 | 155 | 11 | Q9JKT8 | mus pahari  |
| 35 | 116   | 19.9 | 156 | 11 | Q9JKT7 | mus caroli  |
| 36 | 115   | 19.8 | 156 | 11 | Q9JKT5 | mus caroli  |
| 37 | 115   | 19.8 | 156 | 11 | Q9JKT4 | mus caroli  |
| 38 | 115   | 19.8 | 156 | 11 | Q9JKT9 | mus caroli  |
| 39 | 114.5 | 19.7 | 170 | 6  | Q9BEC1 | iragulus ja |
| 40 | 113.5 | 19.5 | 119 | 6  | Q9TSO6 | cercopithec |
| 41 | 113.5 | 19.5 | 119 | 6  | Q9TV32 | gorilla gor |
| 42 | 112.5 | 19.3 | 119 | 6  | Q9TV30 | saguinus oe |
| 43 | 112   | 19.2 | 124 | 6  | Q9TSF2 | bos taurus  |
| 44 | 112   | 19.2 | 156 | 11 | Q9JKT6 | mus musculu |
| 45 | 112   | 19.2 | 156 | 11 | Q8VHS0 | mus musculu |

## ALIGNMENTS

## RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.

AC Q918V8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Onconase Variant rapLRI precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165133; AAF76935.1;  
DR HSSP; P22069; IONC.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_PC; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KW signal.  
FT SIGNAL.  
SO SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 98.5%; Score 573; DB 13; Length 127;  
Best Local Similarity 100.0%; Pred. No. 8.1e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNFIYSRPPVKAICKGIATSKANVLTTS 62  
db 25 DWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNFIYSRPPVKAICKGIATSKANVLTTS 84

|             |   |  |                                    |
|-------------|---|--|------------------------------------|
| Qy          | 63  | EFYLSDCNVTSRPCKYTKLKSTNTFCVTCGNQAPVHFVGGHC             | 105                                |
|             |   |  |                                    |
| Db          | 85  | EFYLSDCNVTSRPCKYTKLKSTNTFCVTCGNQAPVHFVGGHC             | 127                                |
| RESULT 2    |   |  |                                    |
| ID          | Q8UVX5  | PRELIMINARY:   | PRT: 127 AA.                       |
| AC          | Q8UVX5:   |  |                                    |
| DT          | 01-MAR-2002 (TREMBLrel. 20, Created)                                    |  |                                    |
| DT          | 01-MAR-2002 (TREMBLrel. 20, Last sequence update)                       |  |                                    |
| DE          | 01-JUN-2002 (TREMBLrel. 21, Last annotation update)                     |  |                                    |
| DE          | Oncocytase precursor.   |  |                                    |
| GN          | RPR.  |  |                                    |
| OS          | Rana pipiens (Northern leopard frog).                                   |  |                                    |
| OC          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;       |  |                                    |
| OC          | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.      |  |                                    |
| NCBI        | NCBI:TaxID=8404;  |  |                                    |
| RN          | (1)   |  |                                    |
| RP          | SEQUENCE FROM N.A.  |  |                                    |
| RA          | Liao Y.-D., Wang S.-C.;   |  |                                    |
| RT          | "Rana pipiens oncoytase genomic DNA."                                   |  |                                    |
| RL          | Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.                 |  |                                    |
| DR          | EMBL: A8332139; ANL54383.1; -   |  |                                    |
| DR          | InterPro: IPR001427; RNaseA.  |  |                                    |
| DR          | Pfam: PF00074; rnsaeA.1.  |  |                                    |
| DR          | ProDom: PD000535; RNaseA; 1.  |  |                                    |
| DR          | SMART: SM00092; RNase_Pc.1.   |  |                                    |
| DR          | PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.                          |  |                                    |
| KW          | Signal.   |  |                                    |
| FT          | SIGNAL.   |  |                                    |
| SO          | SEQUENCE  | 1 23   | POTENTIAL.                         |
|             |   | 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;              |                                    |
| Query Match |   |  |                                    |
|             | Best Local Similarity   | 94.7%;   | Score 551; DB 13; Length 127;      |
|             | Matches   | 99; Conservative                                       | 2; Mismatches 2; Indels 0; Gaps 0; |
| Qy          | 3   | DMLTQKHLTTRVDCNNITSTLHFCKDKNTFIYSRPEPVKAICGIIASKNVLTTS | 62                                 |
|             |   |  |                                    |
| Db          | 25  | DMLTQKHLTTRVDCNNITSTLHFCKDKNTFIYSRPEPVKAICGIIASKNVLTTS | 84                                 |
|             |   |  |                                    |
| Qy          | 63  | EFYLSDCNVTSRPCKYTKLKSTNTFCVTCGNQAPVHFVGGHC             | 105                                |
|             |   |  |                                    |
| Db          | 85  | EFYLSDCNVTSRPCKYTKLKSTNTFCVTCGNQAPVHFVGGHC             | 127                                |
| RESULT 3    |   |  |                                    |
| ID          | Q9DFY6  | PRELIMINARY:   | PRT: 129 AA.                       |
| AC          | Q9DFY6:   |  |                                    |
| DT          | 01-MAR-2001 (TREMBLrel. 16, Created)                                    |  |                                    |
| DT          | 01-OCT-2001 (TREMBLrel. 18, Last sequence update)                       |  |                                    |
| DE          | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                     |  |                                    |
| DE          | RC-RNaseA ribonuclease precursor.                                       |  |                                    |
| OS          | Rana catesbeiana (Bull frog).   |  |                                    |
| OC          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;       |  |                                    |
| OC          | Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.      |  |                                    |
| NCBI        | NCBI:TaxID=8400;  |  |                                    |
| RN          | (1)   |  |                                    |
| RP          | SEQUENCE FROM N.A.  |  |                                    |
| RA          | TISSUE=LIVER;   |  |                                    |
| RA          | MEDLINE=20512555; PubMed=11058105;                                      |  |                                    |
| RA          | Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; |  |                                    |
| RT          | "Purification and cloning of cytototoxic ribonucleases from Rana        |  |                                    |
| RT          | catesbeiana (bullfrog)."  |  |                                    |
| RL          | Nucleic Acids Res. 28:4097-4104 (2000).                                 |  |                                    |
| RN          | (2)   |  |                                    |
| RP          | SEQUENCE FROM N.A.  |  |                                    |
| RA          | TISSUE=LIVER;   |  |                                    |
| RA          | Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; |  |                                    |
| RT          | Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.                 |  |                                    |
| DR          | EMBL: AF242353; AAG31441.2; -   |  |                                    |
| DR          | HSSP: P22069; IONC.   |  |                                    |

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DR InterPro:IPR001427; RNaseA.  
DR Pfam: PF00074; rnsaeA. 1.  
DR ProDom: PD000535; RNaseA. 1.  
DR SMART: SM00092; RNase_Pc. 1.  
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.  
KW Signal.  
FT SIGNAL. 1 23 POTENTIAL.  
FT CHAIN 24 129 RC-RNASEA RIBONUCLEASE  
SQ SEQUENCE 129 AA; 14724 MW; 826A62892B10ABDA CRC64;  
  
Query Match Best Local Similarity 68.6%; Score 399.5; DB 13; Length 129;  
Matches 70; Conservative 16; Mismatches 17; Indels 1; Gaps 1  
  
QY 3 DWLTFQKKHLTNRDYDCNNIMSTNLPHCKDKNTFIYSRPPEVKAICKGIISKNVLTTS 62  
DQ |||||||:|||||:|:| | :||| | | | | | | | | | | | | | |  
DB 25 DWATFEKKKHLTDWDDCNLMPTSLFDCKDKNTFIYSLPGVKALCRGVISADVLNS 84  
DQ ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 63 EFLYSDCNYSTR-PCRKYLRKSTNFECVGCENQAPVHFVGHC 105  
DQ ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 85 EFLYLACNVKPKRKCYKLKRKSSNRICNGEHELPHVFHFGAGVIC 128  
DQ ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
  
RESULT 4  
Q9DFY8 PRELIMINARY; PRT: 128 AA.  
ID Q9DFY8 AC Q9DFY8;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
OS RC-RNase2 ribonuclease precursor.  
OC Rana catesbeiana (Bull frog).  
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
NCBI_TaxID=8400;  
RN [1]  
RC SEQUENCE FROM N.A.  
PC TISSUE=LIVER;  
RX MEDLINE=20512555; Pubmed=11058105;  
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.-C.;  
RT "Purification and cloning of cytochrome b ribonucleases from Rana  
RL catesbeiana (bullfrog)." ;  
RN Nucleic Acids Res. 28:4097-4104(2000).  
[2]  
RN RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF242553; AACG1439.1; -  
DR HSPB; P22069; IONC.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnsaeA. 1.  
DR ProDom: PD000535; RNaseA. 1.  
DR SMART: SM00092; RNase_Pc. 1.  
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.  
KW Signal.  
FT SIGNAL. 1 23 POTENTIAL.  
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.  
SQ SEQUENCE 128 AA; 14839 MW; 989719CE52053BECC CRC64;  
  
Query Match Best Local Similarity 65.5%; Score 381; DB 13; Length 128;  
Matches 69; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
  
QY 3 DWLTFQKKHLTNRDYDCNNIMSTNLPHCKDKNTFIYSRPPEVKAICKGIISKNVLTTS 62  
DQ |||||||:|||||:|:| | :||| | | | | | | | | | | | | | |  
DB 25 NWETFOKKHLTDTRDVCDAEMKALFDCKOKNTFIYARGRVALLCKNTIVSKNLVS 84  
DQ ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 63 EFLYSDCNYSTR-PCRKYLRKSTNFECVGCENQAPVHFVGHC 105  
DQ ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 85 EFLYSDCNYSTR-PCRKYLRKSTNFECVGCENQAPVHFVGHC 127
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## RESULT 5

Q9DFY7 PRELIMINARY: PRT: 128 AA.  
AC Q9DFY7: 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
RC RNase3 ribonuclease precursor  
OS Rana catesbeiana (bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBL\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog)."  
RL Nucleic Acids Res. 28:4097-4104(2000).  
DR EMBL: AF242551; AAG31440.2;  
DR HSSP: P22069; 10NC;  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnasea; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KW SIGNAL.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.  
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;  
Query Match 52.6%; Score 306; DB 13; Length 128;  
Best Local Similarity 54.4%; Pred. No. 2.6e-27;  
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 3 DWLFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICKGIASKNVLTTS 62  
DB 25 DWLTFQKKHLTDPRKVCDEMKAALFDCKKTFTFYALPGRKALCKNIRDMTDLVSRD 84  
QY 63 EFLSDCNVTSRCKYKLRKSTNFCVTCENQAPVHFGVGHG 105  
DB 85 AFLPQCDRIKLPCHKRLSSSTNTTICTCVNOLEPIHFAGVGC 127

RESULT 6  
Q9DFY5 PRELIMINARY: PRT: 128 AA.  
AC Q9DFY5: 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
RC RNase6 ribonuclease precursor  
OS Rana catesbeiana (bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBL\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog)."  
RL Nucleic Acids Res. 28:4097-4104(2000).  
DR EMBL: AF242551; AAG31442.2;  
DR HSSP: P22069; 10NC;  
DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnasea; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KW SIGNAL.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.  
SQ SEQUENCE 128 AA; 14804 MW; AFE8FD67D266C7C2 CRC64;

Query Match 52.2%; Score 304; DB 13; Length 128;  
Best Local Similarity 53.4%; Pred. No. 4.3e-27;  
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 3 DWLFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICKGIASKNVLTTS 62  
DB 25 DWLTFQKKHLTDPRKVCDEMKAALFDCKKTFTFYALPGRKALCKNIRDMTDLVSRD 84  
QY 63 EFLSDCNVTSRCKYKLRKSTNFCVTCENQAPVHFGVGHG 105  
DB 85 VFYLPQCNRRKLPCHVRLDSTNTTICTCMKELPIHFAGVGC 127

## RESULT 7

Q98SM0 PRELIMINARY: PRT: 133 AA.  
AC Q98SM0: 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
RC RNase A-type ribonuclease rc208 precursor  
OS Rana catesbeiana (bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBL\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21539506; PubMed=11683320;  
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
RT "Rapid diversification of RNase A superfamily ribonuclease from the  
bullfrog, Rana catesbeiana."  
RL J. Mol. Evol. 53:31-38(2001).  
DR EMBL: AF351209; AAK30255.1;  
DR HSSP: P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnasea; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KW SIGNAL.  
FT SIGNAL 1 22 POTENTIAL.  
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.3%; Score 293; DB 13; Length 133;  
Best Local Similarity 49.1%; Pred. No. 8.1e-26;  
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWLFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICKGIASKNV 58  
DB 24 NWATFQCKHITNTNINNTNNTIYVGCGKGVNTFTISSATYKAICTGVI-NMNV 82  
QY 59 LTTSEFLSDC---NVTSRCKYKLRKSTNFCVTCENQAPVHFGVGHG 105  
DB 83 LSTTRFLNLTCTRTSITPRCPPISSRTENNVIYCKCENQAPVHFGVGHG 132

## RESULT 8

Q9PMW7 PRELIMINARY: PRT: 133 AA.  
AC Q9PMW7: 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
RC Ribonuclease precursor

GN RCR.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER.  
 RX MEDLINE=98165825; PubMed=9497370;  
 RA Huang H.C., Wang S.C., Liu Y.J., Lu S.C., Liao Y.D.;  
 RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  
 RT Tissue distribution, cloning, purification, cytotoxicity, and active  
 RT residues for RNase activity."  
 RL J. Biol. Chem. 273:6395-6401(1998).  
 DR EMBL: AF039104; AAD10702.1; -  
 DR HSSP: P11916; IBC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 FT SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 49.3%; Score 287; DB 13; Length 133;  
 Best Local Similarity 49.1%; Pred. No. 3.9e-25;  
 Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNFTIYSRPEPKAICGIIASKNV 58  
 DB 24 NMATFOCKHINTPTIINCNTIMDNINIVGGQCKRVNFTISSATVTKAICGVI-NMNV 82  
 QY 59 LTTSEFYLSDC--VTSRPRCKYKLLKSTNFCVTCENQAPVHVGVC 105  
 DB 83 LSTRFOLDICTRTITRTPPCPYSSRTETNYICVACENQVPHVHAGIGRC 132

## RESULT 9

Q98SM2 PRELIMINARY; PRT; 132 AA.  
 AC Q98SM2:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE RNase A-type ribonuclease rc203 precursor (rc-RNase7 precursor).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539506; PubMed=11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER.  
 RX Liao Y.-D., Tang P.-C., Jeng J.-T.;  
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF351207; AAK30253.1; -  
 DR EMBL: AF359578; AAL87036.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 FT SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 22 POTENTIAL.

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNFTIYSRPEPKAICGIIASKNV 58  
 DB 24 NMATFOCKHINTPTIINCNTIMDNINIVGGQCKRVNFTISSATVTKAICGVI-NMNV 82  
 QY 59 LTTSEFYLSDC--VTSRPRCKYKLLKSTNFCVTCENQAPVHVGVC 105  
 DB 83 LSTRFOLDICTRTITRTPPCPYSSRTETNYICVACENQVPHVHAGIGRC 132

FT CHAIN 23 132 RC-RNASE7.  
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;  
 Query Match 48.3%; Score 281; DB 13; Length 132;  
 Best Local Similarity 47.7%; Pred. No. 1.9e-24;  
 Matches 52; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

QY 4 WLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNFTIYSRPEPKAICGIIASKNV 59  
 DB 25 NMATFOCKHINTPTIINCNTIMDNINIVGGQCKRVNFTISSATVTKAICGVI-NMNV 83  
 QY 60 LTTSEFYLSDC--VTSRPRCKYKLLKSTNFCVTCENQAPVHVGVC 105  
 DB 84 LSTRFOLDICTRTITRTPPCPYSSRTETNYICVACENQVPHVHAGIGRC 132

## RESULT 10

Q98SL9 PRELIMINARY; PRT; 133 AA.  
 AC Q98SL9:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc212 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539506; PubMed=11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, Rana catesbeiana."  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1; -  
 DR HSSP: P11916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea.1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 FT SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 48.3%; Score 281; DB 13; Length 133;  
 Best Local Similarity 47.3%; Pred. No. 1.9e-24;  
 Matches 52; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

## RESULT 11

Q98SL8 PRELIMINARY; PRT; 133 AA.  
 AC Q98SL8:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc218 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE-21539506; PubMed-11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of Rana A superfamily ribonuclease from the  
 bullfrog, *Rana catesbeiana*.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351211; AAK30257.1;  
 DR HSSP: P11916; IBC4.  
 DR InterPro: IPR01427; RNaseA.  
 DR Pfam: PF00074; RNaseA.1.  
 DR Prodom: PD000535; RNaseA.1.  
 DR SMART: SM00092; RNase\_Pc.1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 DR NCBI\_TaxID=8400;  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A4FA5B963 CRC64;

Query Match 47.6%; Score 277; DB 13; Length 133;  
 Best Local Similarity 46.4%; Pred. No. 5.5e-24;  
 Matches 51; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

OY 3 DWLFFOKKHLTNTDVCNNIMSTNLF----HCKDKNTFIYSREPPYKAIKGIASKNV 58  
 ID 098SM1 PRELIMINARY; PRT; 132 AA.  
 AC 098SM1;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc204 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21539506; PubMed-11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of Rana A superfamily ribonuclease from the  
 bullfrog, *Rana catesbeiana*.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF35120E; AAK30254.1;  
 DR HSSP: P11916; IBC4.  
 DR InterPro: IPR01427; RNaseA.  
 DR Pfam: PF00074; RNaseA.1.  
 DR Prodom: PD000535; RNaseA.1.  
 DR SMART: SM00092; RNase\_Pc.1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 DR NCBI\_TaxID=8400;  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 133 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 47.3%; Score 275; DB 13; Length 132;  
 Best Local Similarity 48.2%; Pred. No. 9.2e-24;  
 Matches 53; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

OY 3 DWLFFOKKHLTNTDVCNNIMSTNLF----HCKDKNTFIYSREPPYKAIKGIASKNV 58  
 ID 097738 PRELIMINARY; PRT; 169 AA.  
 AC 097738;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE FR12 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96069863; PubMed-7585965;  
 RA Kinoshita N., Minshull J., Kirschner M.W.;  
 RT "The identification of two novel ligands of the fgf receptor by a  
 yeast screening method and their activity in *Xenopus* development.";  
 RL Cell 83:621-630(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kinoshita N., Kirschner M.W.;

RESULT 13

OY 3 DWLFFOKKHLTNTDVCNNIMSTNLF----HCKDKNTFIYSREPPYKAIKGIASKNV 58  
 ID 097738 PRELIMINARY; PRT; 169 AA.  
 AC 097738;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE FR12 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96069863; PubMed-7585965;  
 RA Kinoshita N., Minshull J., Kirschner M.W.;  
 RT "The identification of two novel ligands of the fgf receptor by a  
 yeast screening method and their activity in *Xenopus* development.";  
 RL Cell 83:621-630(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kinoshita N., Kirschner M.W.;

RESULT 14

